

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/024,806

DATE: 01/15/2002

TIME: 19:04:06

Input Set : A:\35718-241887 SEQLIST.TXT

Output Set: N:\CRF3\01152002\J024806.raw

ENTERED

4 <110> APPLICANT: Zheng, Peizhong  
 5 Li, Chun Ping  
 6 Nichols, Scott E.  
 10 <120> TITLE OF INVENTION: Oar Polynucleotides, Polypeptides and  
 11 Their Use in PHA Production in Plants  
 14 <130> FILE REFERENCE: 35718/241887  
 16 <140> CURRENT APPLICATION NUMBER: US/10/024,806  
 16 <141> CURRENT FILING DATE: 2001-12-19  
 16 <150> PRIOR APPLICATION NUMBER: 60/258,417  
 17 <151> PRIOR FILING DATE: 2000-12-27  
 19 <160> NUMBER OF SEQ ID NOS: 10  
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 1326  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Zea mays  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (157)...(1110)  
 32 <400> SEQUENCE: 1  
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 34 gtcacggctc aaataactccg cctgcatttc caaagcacac tgcctccctt ggcttcccgc 120  
 35 ctctctcttcg gctccttcgc gtcccgaagc cccctc atg gcc acc gcc gcc gcc 174  
 36 Met Ala Thr Ala Ala Ala  
 37 1 5  
 39 acc gca gca gca gca gca gtc tcc tcc ccg gct gcg cgt gga gca gcc 222  
 40 Thr Ala Ala Ala Ala Ala Val Ser Ser Pro Ala Ala Arg Gly Ala Ala  
 41 10 15 20  
 43 ggg gcc gcc gcc gcc tcc cgc cgg ggg ttc gtc acg ttt ggt gga ggc 270  
 44 Gly Ala Ala Ala Ala Ser Arg Arg Gly Phe Val Thr Phe Gly Gly Gly  
 45 25 30 35  
 47 gcc gcc cgc ttc tct ccc acg ctg cgg tcc ggc cgt ggg ttc tct ggt 318  
 48 Ala Ala Arg Phe Ser Pro Thr Leu Arg Ser Gly Arg Gly Phe Ser Gly  
 49 40 45 50  
 51 gtg caa acc cat gtt gct gct gtt gaa caa gca gtt gta aaa gat gct 366  
 52 Val Gln Thr His Val Ala Ala Val Glu Gln Ala Val Val Lys Asp Ala  
 53 55 60 65 70  
 55 acc aag ctg gaa gct cca gtt gtt gtt gtt aca ggt gca tct aga ggg 414  
 56 Thr Lys Leu Glu Ala Pro Val Val Val Val Thr Gly Ala Ser Arg Gly  
 57 75 80 85  
 59 att ggt aag gca act gct cta gcc ctt gga aaa gca gga tgc aag gtt 462  
 60 Ile Gly Lys Ala Thr Ala Leu Ala Leu Gly Lys Ala Gly Cys Lys Val  
 61 90 95 100  
 63 ctg gta aac tat gcc cgg tcc tcg aaa gag gct gaa gag gtc tcc aaa 510  
 64 Leu Val Asn Tyr Ala Arg Ser Ser Lys Glu Ala Glu Glu Val Ser Lys  
 65 105 110 115  
 67 gag att gaa gca tct ggt ggt gag gct atc acc ttc gga gga gat gtt 558

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68 Glu Ile Glu Ala Ser Gly Gly Glu Ala Ile Thr Phe Gly Gly Asp Val
69      120      125      130
71 tca aaa gaa gct gat gta gag tct atg atg aaa gca gct cta gat aaa 606
72 Ser Lys Glu Ala Asp Val Glu Ser Met Met Lys Ala Ala Leu Asp Lys
73 135      140      145      150
75 tgg gga aca ata gat gtg ctg gta aat aat gca ggg att aca cga gac 654
76 Trp Gly Thr Ile Asp Val Leu Val Asn Asn Ala Gly Ile Thr Arg Asp
77      155      160      165
79 aca ttg ttg atg agg atg aag aaa tct cag tgg caa gac gta att gat 702
80 Thr Leu Leu Met Arg Met Lys Lys Ser Gln Trp Gln Asp Val Ile Asp
81      170      175      180
83 ctg aat ctt act ggc gtc ttc ctt tgt aca cag gct gca aca aaa gta 750
84 Leu Asn Leu Thr Gly Val Phe Leu Cys Thr Gln Ala Ala Thr Lys Val
85      185      190      195
87 atg atg aaa aag aga aag gga aaa att atc aac att gca tct gta gtt 798
88 Met Met Lys Lys Arg Lys Gly Lys Ile Ile Asn Ile Ala Ser Val Val
89      200      205      210
91 ggt ctt act ggc aat gtt ggc caa gct aat tat agc gca gcc aag gct 846
92 Gly Leu Thr Gly Asn Val Gly Gln Ala Asn Tyr Ser Ala Ala Lys Ala
93 215      220      225      230
95 gga gtg att ggt ttc aca aaa aca gtt gcc agg gag tat gca agc aga 894
96 Gly Val Ile Gly Phe Thr Lys Thr Val Ala Arg Glu Tyr Ala Ser Arg
97      235      240      245
99 aat atc aat gtg aat gct att gca cca ggg ttc att gca tct gat atg 942
100 Asn Ile Asn Val Asn Ala Ile Ala Pro Gly Phe Ile Ala Ser Asp Met
101      250      255      260
103 act gcc gaa ctt gga gaa gag ctt gag aag aaa atc ttg tca acc att 990
104 Thr Ala Glu Leu Gly Glu Glu Leu Glu Lys Lys Ile Leu Ser Thr Ile
105      265      270      275
107 ccg tta ggg aga tat ggc caa cca gag gaa gtt gca ggg ttg gtc gag 1038
108 Pro Leu Gly Arg Tyr Gly Gln Pro Glu Glu Val Ala Gly Leu Val Glu
109      280      285      290
111 ttc ctg gcc ctt aac ccc gca gct agc tat atg act gga cag gtg ctt 1086
112 Phe Leu Ala Leu Asn Pro Ala Ala Ser Tyr Met Thr Gly Gln Val Leu
113 295      300      305      310
115 aca att gac gga ggg atg gta atg taagatttga gtttagcttga tgcacttcta 1140
116 Thr Ile Asp Gly Gly Met Val Met
117      315
119 ctttttctga gcatttaatg ttgaacaccc ttgttgtgca cgggcgattt tggacaacaa 1200
120 attagtgttg tctctttctt tgtaatactc tctggtaata aatctagcat gtggaatgga 1260
121 agttgaaatc tgggttttcg tgtaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1320
122 aaaaaa 1326
124 <210> SEQ ID NO: 2
125 <211> LENGTH: 318
126 <212> TYPE: PRT
127 <213> ORGANISM: Zea mays
129 <400> SEQUENCE: 2
130 Met Ala Thr Ala Ala Thr Ala Ala Ala Ala Val Ser Ser Pro
131 1 5 10 15

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132 Ala Ala Arg Gly Ala Ala Gly Ala Ala Ala Ser Arg Arg Gly Phe
133      20      25      30
134 Val Thr Phe Gly Gly Gly Ala Ala Arg Phe Ser Pro Thr Leu Arg Ser
135      35      40      45
136 Gly Arg Gly Phe Ser Gly Val Gln Thr His Val Ala Ala Val Glu Gln
137      50      55      60
138 Ala Val Val Lys Asp Ala Thr Lys Leu Glu Ala Pro Val Val Val Val
139 65      70      75      80
140 Thr Gly Ala Ser Arg Gly Ile Gly Lys Ala Thr Ala Leu Ala Leu Gly
141      85      90      95
142 Lys Ala Gly Cys Lys Val Leu Val Asn Tyr Ala Arg Ser Ser Lys Glu
143      100     105     110
144 Ala Glu Glu Val Ser Lys Glu Ile Glu Ala Ser Gly Gly Glu Ala Ile
145      115     120     125
146 Thr Phe Gly Gly Asp Val Ser Lys Glu Ala Asp Val Glu Ser Met Met
147      130     135     140
148 Lys Ala Ala Leu Asp Lys Trp Gly Thr Ile Asp Val Leu Val Asn Asn
149 145     150     155     160
150 Ala Gly Ile Thr Arg Asp Thr Leu Leu Met Arg Met Lys Lys Ser Gln
151      165     170     175
152 Trp Gln Asp Val Ile Asp Leu Asn Leu Thr Gly Val Phe Leu Cys Thr
153      180     185     190
154 Gln Ala Ala Thr Lys Val Met Met Lys Lys Arg Lys Gly Lys Ile Ile
155      195     200     205
156 Asn Ile Ala Ser Val Val Gly Leu Thr Gly Asn Val Gly Gln Ala Asn
157      210     215     220
158 Tyr Ser Ala Ala Lys Ala Gly Val Ile Gly Phe Thr Lys Thr Val Ala
159 225     230     235     240
160 Arg Glu Tyr Ala Ser Arg Asn Ile Asn Val Asn Ala Ile Ala Pro Gly
161      245     250     255
162 Phe Ile Ala Ser Asp Met Thr Ala Glu Leu Gly Glu Glu Leu Glu Lys
163      260     265     270
164 Lys Ile Leu Ser Thr Ile Pro Leu Gly Arg Tyr Gly Gln Pro Glu Glu
165      275     280     285
166 Val Ala Gly Leu Val Glu Phe Leu Ala Leu Asn Pro Ala Ala Ser Tyr
167      290     295     300
168 Met Thr Gly Gln Val Leu Thr Ile Asp Gly Gly Met Val Met
169 305     310     315
172 <210> SEQ ID NO: 3
173 <211> LENGTH: 1286
174 <212> TYPE: DNA
175 <213> ORGANISM: Zea mays
177 <220> FEATURE:
178 <221> NAME/KEY: CDS
179 <222> LOCATION: (115)...(1050)
181 <400> SEQUENCE: 3
182 ccacaccaaa cgtgccaaac ccccaacgcc atcctctata aacggcttcc tcgcgggctc 60
183 cccctcccc tccccgactc ctccccatcg cccatcgccg ccttcgata cttc atg 117
184                                     Met

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185																	1	
187	gcc	gct	gcc	aca	gcc	gcc	gcc	gcc	gcg	ctc	gcc	tcc	cgg	gcg	ggc	ctc	165	
188	Ala	Ala	Ala	Thr	Ala	Ala	Ala	Ala	Ala	Leu	Ala	Ser	Pro	Ala	Gly	Leu		
189				5					10					15				
191	tcc	aca	tcg	ctg	gcg	cgc	cgc	ggc	ctc	gtc	agc	ttc	gca	ccc	gcg	ctc	213	
192	Ser	Thr	Ser	Leu	Ala	Arg	Arg	Gly	Leu	Val	Ser	Phe	Ala	Pro	Ala	Leu		
193				20				25					30					
195	cgc	ccc	ggc	cct	gac	cgc	agc	tct	cgc	gcc	gtc	gcc	ctc	ctc	ggt	gtt	261	
196	Arg	Pro	Gly	Pro	Asp	Arg	Ser	Ser	Arg	Ala	Val	Ala	Leu	Leu	Gly	Val		
197				35				40					45					
199	cga	act	cat	gtc	acg	gct	gtt	gat	caa	gcc	att	gta	aaa	ggt	gat	aca	309	
200	Arg	Thr	His	Val	Thr	Ala	Val	Asp	Gln	Ala	Ile	Val	Lys	Gly	Asp	Thr		
201	50						55					60				65		
203	aag	ttg	gaa	ggt	cct	gtg	gtt	gtt	gtt	act	ggt	gct	tcc	agg	ggg	att	357	
204	Lys	Leu	Glu	Gly	Pro	Val	Val	Val	Val	Thr	Gly	Ala	Ser	Arg	Gly	Ile		
205					70					75						80		
207	gga	aaa	gcc	act	gca	ttg	gct	ctt	gga	aaa	gca	ggc	tgc	aag	gtc	ttg	405	
208	Gly	Lys	Ala	Thr	Ala	Leu	Ala	Leu	Gly	Lys	Ala	Gly	Cys	Lys	Val	Leu		
209				85					90					95				
211	gtg	aat	tat	gct	cga	tct	tca	aag	gag	gct	gaa	gaa	gtc	tcc	aag	gag	453	
212	Val	Asn	Tyr	Ala	Arg	Ser	Ser	Lys	Glu	Ala	Glu	Glu	Val	Ser	Lys	Glu		
213				100				105					110					
215	att	gaa	gca	tct	gga	ggc	cag	gcc	att	acc	ttt	gga	gga	gat	gtt	tcc	501	
216	Ile	Glu	Ala	Ser	Gly	Gly	Gln	Ala	Ile	Thr	Phe	Gly	Gly	Asp	Val	Ser		
217				115			120						125					
219	aaa	gag	gct	gat	gtt	gaa	tct	atg	ata	aaa	gtg	gct	gtt	gat	aca	tgg	549	
220	Lys	Glu	Ala	Asp	Val	Glu	Ser	Met	Ile	Lys	Val	Ala	Val	Asp	Thr	Trp		
221	130					135					140					145		
223	gga	acg	att	gat	gta	cta	gta	aat	aat	gca	gga	atc	aca	cgg	gac	aca	597	
224	Gly	Thr	Ile	Asp	Val	Leu	Val	Asn	Asn	Ala	Gly	Ile	Thr	Arg	Asp	Thr		
225					150					155					160			
227	ttg	ttg	atg	aga	atg	aag	aaa	tca	cag	tgg	caa	gat	gcg	att	gat	ttg	645	
228	Leu	Leu	Met	Arg	Met	Lys	Lys	Ser	Gln	Trp	Gln	Asp	Ala	Ile	Asp	Leu		
229				165					170					175				
231	aat	ctt	aca	ggc	gtt	ttc	ctt	tgc	acg	cag	gct	gca	aca	aaa	gta	atg	693	
232	Asn	Leu	Thr	Gly	Val	Phe	Leu	Cys	Thr	Gln	Ala	Ala	Thr					

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Output Set: N:\CRF3\01152002\J024806.raw

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251 gct gaa ctt ggt gaa gag tta gag aag aaa att ctg tca act att cct 933
252 Ala Glu Leu Gly Glu Glu Leu Glu Lys Lys Ile Leu Ser Thr Ile Pro
253      260      265      270
255 tta ggg cgc tat ggt cgg cca gag gat gta gca ggc ctg gtg gaa ttc 981
256 Leu Gly Arg Tyr Gly Arg Pro Glu Asp Val Ala Gly Leu Val Glu Phe
257      275      280      285
259 tta gcc ctc agc cct gct gca agc tac atc act gga cag gtc ctc acc 1029
260 Leu Ala Leu Ser Pro Ala Ala Ser Tyr Ile Thr Gly Gln Val Leu Thr
261 290      295      300      305
263 atc gat gga gga atg gta atg taaggcttcg aatctgtgcc gctggcctct 1080
264 Ile Asp Gly Gly Met Val Met
265      310
267 aatgtgtcgc agaaaaaaaa tgtaattcag ttttttgagt gtcattttta aggggtggtt 1140
268 tcttttgtcc gcagcggttt gtggtatagt acagtttggt tcgaaggag agttgatact 1200
269 agaaatttgc acacgtatag ttagcttaat ttctttgcga ttggccgatt gctccaaaaa 1260
270 aaaaaaaaaa aaaaaaaaaa aaaaaa 1286
272 <210> SEQ ID NO: 4
273 <211> LENGTH: 312
274 <212> TYPE: PRT
275 <213> ORGANISM: Zea mays
277 <400> SEQUENCE: 4
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279 1      5      10      15
280 Leu Ser Thr Ser Leu Ala Arg Arg Gly Leu Val Ser Phe Ala Pro Ala
281      20      25      30
282 Leu Arg Pro Gly Pro Asp Arg Ser Ser Arg Ala Val Ala Leu Leu Gly
283      35      40      45
284 Val Arg Thr His Val Thr Ala Val Asp Gln Ala Ile Val Lys Gly Asp
285      50      55      60
286 Thr Lys Leu Glu Gly Pro Val Val Val Val Thr Gly Ala Ser Arg Gly
287 65      70      75      80
288 Ile Gly Lys Ala Thr Ala Leu Ala Leu Gly Lys Ala Gly Cys Lys Val
289      85      90      95
290 Leu Val Asn Tyr Ala Arg Ser Ser Lys Glu Ala Glu Glu Val Ser Lys
291      100      105      110
292 Glu Ile Glu Ala Ser Gly Gly Gln Ala Ile Thr Phe Gly Gly Asp Val
293      115      120      125
294 Ser Lys Glu Ala Asp Val Glu Ser Met Ile Lys Val Ala Val Asp Thr
295      130      135      140
296 Trp Gly Thr Ile Asp Val Leu Val Asn Asn Ala Gly Ile Thr Arg Asp
297 145      150      155      160
298 Thr Leu Leu Met Arg Met Lys Lys Ser Gln Trp Gln Asp Ala Ile Asp
299      165      170      175
300 Leu Asn Leu Thr Gly Val Phe Leu Cys Thr Gln Ala Ala Thr Lys Val
301      180      185      190
302 Met Met Lys Lys Lys Lys Gly Arg Ile Ile Asn Ile Ala Ser Val Val
303      195      200      205
304 Gly Leu Thr Gly Asn Ala Gly Gln Ala Asn Tyr Ala Ala Ala Lys Ala
305      210      215      220

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/024,806

DATE: 01/15/2002

TIME: 19:04:07

Input Set : A:\35718-241887 SEQLIST.TXT

Output Set: N:\CRF3\01152002\J024806.raw

L:16 M:270 C: Current Application Number differs, Replaced Current Application No  
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date